



PCT10

RAW SEQUENCE LISTING

DATE: 08/13/2002

PATENT APPLICATION: US/10/088,744

TIME: 16:40:25

Input Set : A:\Igs4n21.app

Output Set: N:\CRF4\08132002\J088744.raw

3 <110> APPLICANT: SOLVAY PHARMACEUTICALS B.V.
 5 <120> TITLE OF INVENTION: Novel human G-protein coupled Receptor
 7 <130> FILE REFERENCE: SPW99.06/HA 00.19
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/088,744
 C--> 10 <141> CURRENT FILING DATE: 2002-07-22
 12 <160> NUMBER OF SEQ ID NOS: 34
 14 <170> SOFTWARE: PatentIn Ver. 2.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 1658
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Homo sapiens
 21 <220> FEATURE:
 22 <221> NAME/KEY: CDS
 23 <222> LOCATION: (55)..(1299)
 24 <223> OTHER INFORMATION: IGS4A long version
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 28 Met
 29 1
 31 tca ggg atg gaa aaa ctt cag aat gct tcc tgg atc tac cag cag aaa 105
 32 Ser Gly Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys
 33 5 10 15
 35 cta gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg 153
 36 Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu
 37 20 25 30
 39 gcc ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct 201
 40 Ala Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser
 41 35 40 45
 43 gtg gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg 249
 44 Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu
 45 50 55 60 65
 47 gtg tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac 297
 48 Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn
 49 70 75 80
 51 tac tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt 345
 52 Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu
 53 85 90 95
 55 gga atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg 393
 56 Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu
 57 100 105 110
 59 ttc ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg 441
 60 Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val
 61 115 120 125

ENTERED

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63 tgc ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac 489
64 Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr
65 130 135 140 145
67 gtg gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc 537
68 Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg
69 150 155 160
71 cgg gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc 585
72 Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe
73 165 170 175
75 tcc ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc 633
76 Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro
77 180 185 190
79 aat ggg tcc ctg gtc cca ggt tgg gcc acc tgt acg gtc atc aag ccc 681
80 Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro
81 195 200 205
83 atg tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac 729
84 Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr
85 210 215 220 225
87 ctc ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc 777
88 Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu
89 230 235 240
91 aga cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat 825
92 Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn
93 245 250 255
95 att caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg 873
96 Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu
97 260 265 270
99 gtc tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc 921
100 Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu
101 275 280 285
103 ttc ttc agc ttt gtg gag gag tgg agt gaa tcc ctg gct gct gtg ttc 969
104 Phe Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val Phe
105 290 295 300 305
107 aac ctc gtc cat gtg gtg tca ggt gtc ttc ttc tac ctg agc tca gct 1017
108 Asn Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser Ala
109 310 315 320
111 gtc aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca 1065
112 Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala
113 325 330 335
115 ttc cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat 1113
116 Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His
117 340 345 350
119 gac cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc 1161
120 Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys
121 355 360 365
123 cac ttt gtg gag ctg acc gaa gat ata ggt ccc caa ttc cca tgt cag 1209
124 His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys Gln
125 370 375 380 385
127 tca tcc atg cac aac tct cac ctc cca aca gcc ctc tct agt gaa cag 1257

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128 Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu Gln
129          390          395          400
131 atg tca aga aca aac tat caa agc ttc cac ttt aac aaa acc          1299
132 Met Ser Arg Thr Asn Tyr Gln Ser Phe His Phe Asn Lys Thr
133          405          410          415
135 tgaattcttt cagagctgac tctcctctat gcctcaaaac ttcagagagg aacatcccat 1359
137 aatgtatgcc ttctcatatg atattagaga ggtagaatgg ctcttacaac tcatgtaccc 1419
139 attgctagtt tttttttttt aataaacgtg aaaactgaga gttagatctg gtttcaaaac 1479
141 ccaagactgc ctgattttta gttatctttc cactatccta actgcctcat gccctttcac 1539
143 tagttcatgc caagaacgtg actggaaagg catggcacct ataccttgat taatttccat 1599
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150 <212> TYPE: PRT
151 <213> ORGANISM: Homo sapiens
153 <400> SEQUENCE: 2
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155   1          5          10          15
157 Lys Leu Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr
158          20          25          30
160 Leu Ala Phe Leu Cys Gly Pro Arg Ser His Phe Phe Leu Pro Val
161          35          40          45
163 Ser Val Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val
164          50          55          60
166 Leu Val Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr
167 65          70          75          80
169 Asn Tyr Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu
170          85          90          95
172 Leu Gly Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe
173          100          105          110
175 Leu Phe Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr
176          115          120          125
178 Val Cys Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg
179          130          135          140
181 Tyr Val Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg
182 145          150          155          160
184 Arg Arg Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu
185          165          170          175
187 Phe Ser Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe
188          180          185          190
190 Pro Asn Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys
191          195          200          205
193 Pro Met Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe
194          210          215          220
196 Tyr Leu Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala
197 225          230          235          240
199 Leu Arg Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala
200          245          250          255
202 Asn Ile Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val

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203          260          265          270
205 Leu Val Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg
206          275          280          285
208 Leu Phe Phe Ser Phe Val Glu Trp Ser Glu Ser Leu Ala Ala Val
209          290          295          300
211 Phe Asn Leu Val His Val Ser Gly Val Phe Phe Tyr Leu Ser Ser
212 305          310          315          320
214 Ala Val Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala
215          325          330          335
217 Ala Phe Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln
218          340          345          350
220 His Asp Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu
221          355          360          365
223 Cys His Phe Val Glu Leu Thr Glu Asp Ile Gly Pro Gln Phe Pro Cys
224          370          375          380
226 Gln Ser Ser Met His Asn Ser His Leu Pro Thr Ala Leu Ser Ser Glu
227 385          390          395          400
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230          405          410          415
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 1658
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (64)..(1299)
242 <223> OTHER INFORMATION: IGS4A short version
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248 Met Glu Lys Leu Gln Asn Ala Ser Trp Ile Tyr Gln Gln Lys Leu
249 1 5 10 15
251 gaa gat cca ttc cag aaa cac ctg aac agc acc gag gag tat ctg gcc 156
252 Glu Asp Pro Phe Gln Lys His Leu Asn Ser Thr Glu Glu Tyr Leu Ala
253 20 25 30
255 ttc ctc tgc gga cct cgg cgc agc cac ttc ttc ctc ccc gtg tct gtg 204
256 Phe Leu Cys Gly Pro Arg Arg Ser His Phe Phe Leu Pro Val Ser Val
257 35 40 45
259 gtg tat gtg cca att ttt gtg gtg ggg gtc att ggc aat gtc ctg gtg 252
260 Val Tyr Val Pro Ile Phe Val Val Gly Val Ile Gly Asn Val Leu Val
261 50 55 60
263 tgc ctg gtg att ctg cag cac cag gct atg aag acg ccc acc aac tac 300
264 Cys Leu Val Ile Leu Gln His Gln Ala Met Lys Thr Pro Thr Asn Tyr
265 65 70 75
267 tac ctc ttc agc ctg gcg gtc tct gac ctc ctg gtc ctg ctc ctt gga 348
268 Tyr Leu Phe Ser Leu Ala Val Ser Asp Leu Leu Val Leu Leu Leu Gly
269 80 85 90 95
271 atg ccc ctg gag gtc tat gag atg tgg cgc aac tac cct ttc ttg ttc 396
272 Met Pro Leu Glu Val Tyr Glu Met Trp Arg Asn Tyr Pro Phe Leu Phe

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273		100		105		110		
275	ggg ccc gtg ggc tgc tac ttc aag acg gcc ctc ttt gag acc gtg tgc							444
276	Gly Pro Val Gly Cys Tyr Phe Lys Thr Ala Leu Phe Glu Thr Val Cys							
277		115		120		125		
279	ttc gcc tcc atc ctc agc atc acc acc gtc agc gtg gag cgc tac gtg							492
280	Phe Ala Ser Ile Leu Ser Ile Thr Thr Val Ser Val Glu Arg Tyr Val							
281		130		135		140		
283	gcc atc cta cac ccg ttc cgc gcc aaa ctg cag agc acc cgg cgc cgg							540
284	Ala Ile Leu His Pro Phe Arg Ala Lys Leu Gln Ser Thr Arg Arg Arg							
285		145		150		155		
287	gcc ctc agg atc ctc ggc atc gtc tgg ggc ttc tcc gtg ctc ttc tcc							588
288	Ala Leu Arg Ile Leu Gly Ile Val Trp Gly Phe Ser Val Leu Phe Ser							
289	160		165		170		175	
291	ctg ccc aac acc agc atc cat ggc atc aag ttc cac tac ttc ccc aat							636
292	Leu Pro Asn Thr Ser Ile His Gly Ile Lys Phe His Tyr Phe Pro Asn							
293		180		185		190		
295	ggg tcc ctg gtc cca ggt tgc gcc acc tgt acg gtc atc aag ccc atg							684
296	Gly Ser Leu Val Pro Gly Ser Ala Thr Cys Thr Val Ile Lys Pro Met							
297		195		200		205		
299	tgg atc tac aat ttc atc atc cag gtc acc tcc ttc cta ttc tac ctc							732
300	Trp Ile Tyr Asn Phe Ile Ile Gln Val Thr Ser Phe Leu Phe Tyr Leu							
301		210		215		220		
303	ctc ccc atg act gtc atc agt gtc ctc tac tac ctc atg gca ctc aga							780
304	Leu Pro Met Thr Val Ile Ser Val Leu Tyr Tyr Leu Met Ala Leu Arg							
305		225		230		235		
307	cta aag aaa gac aaa tct ctt gag gca gat gaa ggg aat gca aat att							828
308	Leu Lys Lys Asp Lys Ser Leu Glu Ala Asp Glu Gly Asn Ala Asn Ile							
309	240		245		250		255	
311	caa aga ccc tgc aga aaa tca gtc aac aag atg ctg ttt gtc ttg gtc							876
312	Gln Arg Pro Cys Arg Lys Ser Val Asn Lys Met Leu Phe Val Leu Val							
313		260		265		270		
315	tta gtg ttt gct atc tgt tgg gcc ccg ttc cac att gac cga ctc ttc							924
316	Leu Val Phe Ala Ile Cys Trp Ala Pro Phe His Ile Asp Arg Leu Phe							
317		275		280		285		
319	ttc agc ttt gtg gag gag tgg agt gaa tcc ctg gct gct gtg ttc aac							972
320	Phe Ser Phe Val Glu Glu Trp Ser Glu Ser Leu Ala Ala Val Phe Asn							
321		290		295		300		
323	ctc gtc cat gtg gtg tca ggt gtc ttc ttc tac ctg agc tca gct gtc							1020
324	Leu Val His Val Val Ser Gly Val Phe Phe Tyr Leu Ser Ser Ala Val							
325		305		310		315		
327	aac ccc att atc tat aac cta ctg tct cgc cgc ttc cag gca gca ttc							1068
328	Asn Pro Ile Ile Tyr Asn Leu Leu Ser Arg Arg Phe Gln Ala Ala Phe							
329	320		325		330		335	
331	cag aat gtg atc tct tct ttc cac aaa cag tgg cac tcc cag cat gac							1116
332	Gln Asn Val Ile Ser Ser Phe His Lys Gln Trp His Ser Gln His Asp							
333		340		345		350		
335	cca cag ttg cca cct gcc cag cgg aac atc ttc ctg aca gaa tgc cac							1164
336	Pro Gln Leu Pro Pro Ala Gln Arg Asn Ile Phe Leu Thr Glu Cys His							
337		355		360		365		

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/088,744

DATE: 08/13/2002
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Input Set : A:\Igs4n21.app
Output Set: N:\CRF4\08132002\J088744.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 21,24

Seq#:14; N Pos. 22,25,28